

Each row represents a different modification site identified. The same peptide is listed twice for site ids 31 and 32 and site ids 36 and 37 because the peptide was found to be modified twice. In addition, the same modification site might be found on overlapping peptides, but only the best identified peptide is listed.

A. Leading proteins: Uniprot identifiers of proteins where modification occurred

B. Gene name: Gene names of proteins where modification occurred

C. Positions within proteins: Position of modification in leading proteins

D. PEP: Posterior error probability of identification as calculated by MaxQuant

E. Modified sequence: Peptide sequence best identifying site of modification, actual site denoted as (gl)

F. GlyGly (K) Probabilities: Site localization probability within peptide as calculated by MaxQuant

G. Samples: Experiments where modification was detected

H. Previously Identified: Studies that had previously identified modification site

a: Systematic Approach for Validating the Ubiquitinated Proteome, Anal Chem, Seyfried et al (2008)

b: A perturbed ubiquitin landscape distinguishes between ubiquitin in trafficking and in proteolysis, MCP, Ziv et al (2011)

c: A proteomics approach to understanding protein ubiquitination, Nat Biotech, Peng et al (2003)

d: A subset of membrane-associated proteins is ubiquitinated in response to mutations in the endoplasmic reticulum degradation machinery, PNAS, Hitchcock et al (2003)

I. id: Modification site identifier for cross-referencing